REMARKS

Reconsideration of the rejections set forth in the Final Office Action mailed on October 20, 2006, is respectfully requested. Claim 24 has been canceled. Claims 1, 6, 9-14, 20-21, 23, 25, and 27 have been amended. Support for these amendments can be found in the specification at, e.g., page 2, lines 13-15; page 5, lines 8-14; page 5, line 28 - page 7, line 14; page 8, lines 14-31; page 9, line 20 - page 11, line 18; page 11, line 26 - page 12, line 15; page 16, lines 6-22; page 17, lines 10-18; Therefore, these amendments have been made without the addition of new matter. Claims 1, 5-14, 17-23, 25, and 27 remain pending.

Specification

Applicants have corrected typographical errors in the paragraph beginning on page 29, line 30.

Claim Objections

Claim 1 was objected to for the following informality: "and" between the second providing step and the second hybridizing step. Applicants have amended claim 1 to delete the "and."

Claim 23 or 27 is objected to for the following informalities: there should be the word "and" between the providing and hybridizing steps. Applicants have amended these claims to add the word "and."

35 U.S.C. § 112

Claims 1, 5-9, 17-20, 22-25, and 27 were rejected under 35 U.S.C. 112, first paragraph, as allegedly failing to comply with the written description requirement. Applicants have amended the claims to recite "[a] method for detecting a polymorphism related to a genetic disease in a patient sample nucleic acid." Support for this amendment can be found in the specification at, e.g., page 2, lines 13-15,page 5, lines 8-14, page 5, line 28 - page 6, line 28, page 11, line 26 - page 12, line 15; page 17, lines 10-18. Therefore, no new matter was added with this amendment.

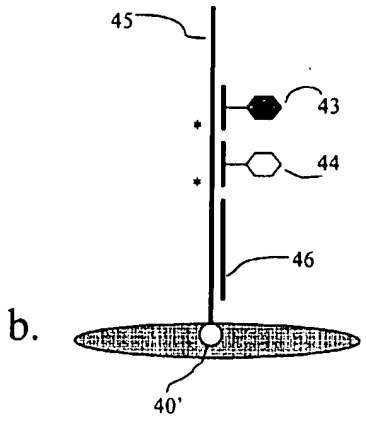
Claims 1, 24, and 25 were rejected under 35 U.S.C. § 112, first paragraph, because the specification allegedly does not reasonably provide enablement for detecting any kind of genetic disease. Applicants have amended claim 1 to specify that the patient sample have a first and a second loci having first and second polymorphisms, respectively, that are related to the genetic disease being detected. Furthermore, a detectable discriminator that is specific for the second polymorphism, which is related to the genetic disease, is hybridized to the second loci containing the second polymorphism related to the genetic disease. The detectable discriminator is then detected to determine the presence of the second polymorphism. Therefore, Applicants respectfully assert that claim 1, as amended, clearly recites how the detectable discriminator can be used to detect the genetic disease. Applicants respectfully request withdrawal of the rejections and reconsideration of the claims as amended.

Art Rejections

Claims 1, 5-9, 17-20, 22-24, and 27 have been rejected under 35 U.S.C. § 102(e) as allegedly anticipated by Nerenberg et al. (USP 6,468,742). Claim 25 was rejected under 35 U.S.C. § 103(a) as allegedly unpatentable over Nerenberg et al. in view of Song et al. (USP 6,451,526).

The Examiner has taken the position that "the at least one stabilizer oligonucleotide" described in Nerenberg is a "blocker ... selected for particular loci," as previously required by claim 1. Applicants respectfully assert that the Examiner has failed to show that Nerenberg teaches providing "*a blocker that is complementary to the first loci containing the first polymorphism related to the genetic disease*," as required in amended claim 1. Although the stabilizer described in Nerenberg is complementary to a portion of the amplification product, it is not complementary to "*the first loci containing the first polymorphism related to the genetic disease.*" As stated in Nerenberg, "[t]he stabilizer oligomer 33 is generally a 30-mer that is 100% complementary to both wild type and mutant alleles. This stabilizer directly abuts the polymorphism site on the target amplicon such that when a perfectly matched mutant reporter 34 or wild-type 35 is added to the system, base-stacking will be present." (emphasis added, Col. 16, lines 30-36). Because the stabilizer "directly abuts" the loci, it is not complementary to the loci, but rather is complementary to a sequence near the loci. Additionally, because the stabilizer is "100% complementary to both wild type and mutant alleles," the stabilizer must not be hybridizing with the portion of the amplification product that contains the loci (i.e., the polymorphism that makes the mutant different from the wild type). As stated previously, the stabilizer is hybridizing with a portion of the amplification products that is common to both.

Furthermore, where Nerenberg describes multiple closely spaced SNPs (see Fig. 4B below), the reporter probes are simultaneously bonded to the genetic locus in order to provide multiple base-stacking energies.



(See Col. 21, line 53 - Col. 22, line 6 "Fig. 4 sets forth a format wherein multiple SNP containing reporter probes are used with one another to provide multiple base-stacking energies. ... In this format, the reporter probes are base-stacked against a stabilizer oligo and each of the reporters may be labeled with a different fluorophore specific for an allele that occurs at these sites.") Therefore, a blocker is not hybridized "with the first loci, wherein the second loci is unblocked," as required by the claims because all of the SNPs present are simultaneously detected.

Claims 5-9, 17-20, 22-23, 25, and 27 depend from claim 1 and are patentably distinct for the same reasons as applicable to claim 1. Therefore, Applicants respectfully request withdrawal of the rejections and reconsideration of the claims as amended.

Favorable action on the merits of the claims is therefore earnestly solicited. If any issues remain, please contact Applicant's undersigned representative at (949) 760-9600. The

Commissioner is hereby authorized to charge any additional fees that may be required to Deposit Account No. 50-2862.

Respectfully submitted,
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